FILE 'CAPLUS' ENTERED AT 15:16:49 ON 08 JAN 2004
L1 116 (AFFINIT? (5A) PURIF?) (S) (MASS (3A) SPECTR?)
L2 2 L1 AND (HYDROPHOB? OR HYDROPHIL?)
L3 57 (AFFINIT? (5A) PURIF?) (6A) (MASS (3A) SPECTR?)
L4 0 HUTCHENS/AU AND (MASS (3A) SPECTR?)
L5 117 HUTCHENS T?/AU
L6 36 L5 AND (MASS (3A) SPECTR?)
L7 16 L6 AND AFFINIT?
L8 368 AFFINITY (3A) MASS(3A) SPECTR?
L9 66 L8 AND PURIF?
L10 1 PURIF? (6A) (MALDI (2A) TARGET)
L11 1379 PURIF? (6A) (MASS (3A) SPECTR?)
L12 46 L11 AND ((PURIF? OR AFFINITY) (S) (TARGET OR SUBSTRATE))
L13 588 AFFINITY (6A) (MASS (2A) SPECTR?)
L14 2 L13 AND (PURIF? (5A) DIRECT?)
L15 12 L13 AND (HYDROPHOB? OR HYDROPHIL?)

L3 ANSWER 24 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:174891 CAPLUS
DOCUMENT NUMBER: 139:130074
TITLE: "Affinity purification-mass spectrometry. Powerful tools for the characterization of protein complexes"
AUTHOR(S): *Bauer, Andreas; Kuster, Bernhard*
CORPORATE SOURCE: Cellzome AG, Heidelberg, 69117, Germany
SOURCE: **European Journal of Biochemistry (2003), 270(4), 570-578**
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Blackwell Publishing Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review. Multi-protein complexes are emerging as important entities of biol. activity inside cells that serve to create functional diversity by contextual combination of gene products and, at the same time, organize the large number of different proteins into functional units. Many a time, when studying protein complexes rather than individual proteins, the biol. insight gained has been fundamental, particularly in cases in which proteins with no previous functional annotation could be placed into a functional context derived from their "mol. environment". In this minireview, we summarize the current state of the art for the retrieval of multi-protein complexes by affinity purification and their anal. by mass spectrometry. The advances in technol. made over the past few years now enable the study of protein complexes on a proteomic scale and it can be anticipated that the knowledge gathered from such projects will fuel drug target discovery and validation pipelines and that the technol. is also going to prove valuable in the emerging field of systems biol. REFERENCE COUNT: 35

L3 ANSWER 38 OF 57 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 2002:52067 CAPLUS
DOCUMENT NUMBER: 136:196093
TITLE: Novel Interactions of Saccharomyces cerevisiae Type 1 Protein Phosphatase Identified by Single-Step Affinity Purification and Mass Spectrometry
AUTHOR(S): Walsh, Edmund P.; Lamont, Douglas J.; Beattie, Kenneth A.; Stark, Michael J. R.
CORPORATE SOURCE: School of Life Sciences Biocentre, University of Dundee, Dundee, DD1 5EH, UK
SOURCE: Biochemistry (2002), 41(7), 2409-2420
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The catalytic subunit of Saccharomyces cerevisiae type 1 protein phosphatase (PP1C) is encoded by the essential gene GLC7 and is involved in regulating diverse cellular processes. To identify potential regulatory or targeting subunits of yeast PP1C, we tagged Glc7p at its amino terminus with protein A and affinity-purified Glc7p protein complexes from yeast. The purified proteins were separated by SDS-PAGE and identified by peptide mass fingerprint anal. using matrix-assisted laser desorption/ionization (MALDI) mass spectrometry. To confirm the accuracy of our identifications, peptides from some of the proteins were also sequenced using high-performance liquid chromatog. (HPLC) coupled to tandem mass spectrometry. Only four of the Glc7p-associated proteins that we identified (Mhp1p, Bni4p, Ref2p, and Sds22p) have previously been shown to interact with Glc7p, and multiple components of the CPF (cleavage and polyadenylation factor) complex involved in mRNA 3'-end processing were present as major components in the Glc7p-associated protein fraction. To confirm the interaction of Glc7p with this complex, we used the same approach to purify and characterize the components of the yeast CPF complex using protein A-tagged Pta1p. Six known components of the yeast (CPF) complex, together with Glc7p, were identified among the Pta1p-associated polypeptides using peptide mass fingerprint anal. Thus Glc7p is a novel component of the CPF complex and may therefore be involved regulating mRNA 3'-end processing. REFERENCE COUNT: 60

7 ANSWER 1 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:797242 CAPLUS
DOCUMENT NUMBER: 130:179479
TITLE: Direct detection and quantitative determination of bovine lactoferricin and lactoferrin fragments in human gastric contents by affinity mass spectrometry
AUTHOR(S): Kuwata, Hidefumi; Yip, Tai-Tung; Yip, Christine L.; Tomita, Mamoru; Hutchens, T. William
CORPORATE SOURCE: Department of Food Science and Technology, University of California, Davis, Davis, CA, USA
SOURCE: Advances in Experimental Medicine and Biology (1998), 443(Advances in Lactoferrin Research), 23-32
CODEN: AEMBAP; ISSN: 0065-2598
PUBLISHER: Plenum Publishing Corp.

DOCUMENT TYPE: Journal
LANGUAGE: English
AB Lactoferricin (Lfcin) is a bioactive fragment of lactoferrin derived from the bactericidal and putative lymphocyte receptor binding domain(s) located within the N-lobe of lactoferrin. Although known to be liberated from at least three species of lactoferrin, conditions leading to Lfcin generation in vivo and factors affecting its distribution are still not known. Recently, we have developed a method of surface-enhanced laser desorption/ionization (SELDI) affinity mass spectrometry using Bu terminal groups for surface-enhanced affinity capture (SEAC) to quantify not only Lfcin generated in vivo but also other lactoferrin fragments. Unlike previous efforts to detect lactoferrin and Lfcin with specific antibodies, the SELDI affinity assay distinguished lactoferrin, lactoferrin fragments, Lfcin and unrelated peptides without their interference with each other. To evaluate Lfcin generation in vivo, the exptl. design involved feeding 200 mL of 10 mg/mL (1.22+10-4 mol/L) bovine lactoferrin to an adult. Gastric contents were recovered 10 min after ingestion. Lfcin produced in vivo was directly captured by the SEAC device. The amount of Lfcin in the gastric contents was 16.91±2.65 <SYM109>g/mL (5.350±0.838+10-6 mol/L). However, a large proportion of the ingested lactoferrin was not completely digested. Lactoferrin fragments containing the Lfcin region were analyzed by in situ hydrolysis with pepsin after being captured by the SEAC device. As much as 5.740±0.702+10-5 mol/L of the partially degraded lactoferrin fragments were found to contain the Lfcin region, including peptide domains 17-43, 17-44, 12-44, 9-58, and 16-76 of bovine lactoferrin. These results show that bovine Lfcin can be produced in the human stomach after ingestion of an infant formula supplemented with bovine lactoferrin. It is now important to determine whether Lfcin is generated in the intestinal tract of formula-fed and breast-fed infants,and geriatric patients consuming foods enriched with lactoferrin. REFERENCE COUNT: 22

L7 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:271835 CAPLUS
DOCUMENT NUMBER: 129:38238
TITLE: Bactericidal domain of lactoferrin: detection, quantitation, and characterization of lactoferricin in serum by SELDI affinity mass spectrometry
AUTHOR(S): Kuwata, Hidefumi; Yip, Tai-Tung; Yip, Christine L.; Tomita, Mamoru; Hutchens, T. William
CORPORATE SOURCE: Department of Food Science and Technology, University of California, Davis, CA, 95616, USA
SOURCE: Biochemical and Biophysical Research Communications (1998), 245(3), 764-773
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Lactoferricin is a bioactive peptide fragment (3169 Da) derived from lactoferrin (80 kDa) that contains the bactericidal domain and the lymphocyte receptor-binding domain of lactoferrin. Although lactoferricin has been produced from lactoferrin by proteolytic digestion in vitro, its natural occurrence and distribution in vivo are still not clear, in part

because of the absence of a suitable detection means. Surface-enhanced laser desorption/ionization (SELDI) was used to detect and characterize lactoferricin by affinity mass spectrometry. Human, porcine, and bovine lactoferricin in unfractionated serum samples were found to bind specifically to ligands presenting a terminal Bu group. SELDI was used to detect and quantify each species of lactoferricin in a manner that was independent of the presence of intact lactoferrin, partially degraded lactoferrin, and lactoferrin peptides containing the lactoferricin peptide sequence. The limit of detection of bovine lactoferricin in serum was as low as 200 pg/mL. The FKCRRWQWR-homoserine/- homoserine lactone moiety of bovine lactoferricin, which includes the complete antimicrobial center (i.e., RRWQWR), was shown to be responsible for interaction with the Bu group. The SELDI procedure defined here is the only mol. recognition tool known to date that is capable of distinguishing the multi-functional lactoferricin domain located within structurally related but distinct forms of lactoferrin and its metabolic fragments. Enabling the direct quantitation of lactoferricin produced in vivo opens new opportunities to evaluate lactoferrin function.
REFERENCE COUNT: 10

L7 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:146549 CAPLUS
DOCUMENT NUMBER: 128:138323
TITLE: Method and apparatus for desorption and ionization of analytes
INVENTOR(S): Hutchens, T. William; Yip, Tai-Tung
PATENT ASSIGNEE(S): Baylor College of Medicine, USA
SOURCE: U.S., 64 pp., Cont.-in-part of U.S. Ser. No. 68,896.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
PATENT NO. KIND DATE APPLICATION NO. DATE
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US 5719060 A 19980217 US 1995-483357 19950607 CA 2163426 AA 19941208 CA 1994-2163426 19940527 JP 2000131285 A2 20000512 JP 1999-237646 19940527 JP 3457228 B2 20031014 EP 1347493 A2 20030924 EP 2003-12514 19940527 US 5894063 A 19990413 US 1997-785637 19970117
US 6027942 A 20000222 US 1997-785636 19970117
US 2001023074 A1 20010920 US 1998-123253 19980727
US 2002155620 A1 20021024 US 2000-742494 20001220
US 6528320 B2 20030304 US 2001014479 A1 20010816 US 2001-809657 20010315 JP 2004004124 A2 20040108 JP 2003-292545 20030812
PRIORITY APPLN. INFO.: US 1993-68896 A2 19930528 EP 1994-919287 A3 19940527 JP 1994-501011 A3 19940527 JP 1995-501011 A3 19940527
AB This invention relates generally to methods and apparatus for desorption and ionization of analytes for the purpose of subsequent scientific anal. by such methods, for example, as mass spectrometry or biosensors. More specifically, this invention relates to the field of mass spectrometry, especially to the type of matrix-assisted laser desorption/ ionization, time-of-flight mass spectrometry used to analyze macromols., such as proteins or biomols. Most specifically, this invention relates to the sample probe geometry,

sample probe composition, and sample probe surface chemistries that enable the selective capture and desorption of analytes, including intact macromols., directly from the probe surface into the gas (vapor) phase without added chemical matrix.
REFERENCE COUNT: 14

L7 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:562079 CAPLUS
DOCUMENT NUMBER: 127:217309
TITLE: "Surface-enhanced laser desorption/ionization (SELDI): probe surfaces enhanced for affinity capture (SEAC) of energy absorbing molecules (EAM) for neat desorption (SEND) of intact biopolymers"
AUTHOR(S): *Hutchens, T. William; Yip, Tai-Tung; Ching, Jesus; Bardel, Patrick*
CORPORATE SOURCE: Department of Food Science and Technology, University of California, Davis, CA, 95616, USA
SOURCE: **Microbeam Analysis, Proceedings of the Annual Conference of the Microbeam Analysis Society, 29th, Breckenridge, Colo., Aug. 6-11, 1995 (1995), 41-42. Editor(s): Etz, Edgar S. VCH: New York, N. Y.**
CODEN: 64WPAL
DOCUMENT TYPE: Conference
LANGUAGE: English
AB This report focuses on new solid-phase and solution chemistries to build and assemble SEND (surfaces enhanced for neat desorption) probe surfaces. A new hybrid probe surface design is presented. Probe elements with SEND were constructed from SEAC devices designed to bind EAM. An example is the attachment of thiosalicylic acid as the EAM to a probe element surface by means of covalently attached iminodiacetate-Cu(II) as the affinity capture mol. Analytes such as synthetic peptides or myoglobin were analyzed by SELDI time-of-flight mass spectrometry.

L7 ANSWER 7 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:323722 CAPLUS
DOCUMENT NUMBER: 127:31077
TITLE: "Affinity mass spectrometry. Probes with surfaces enhanced for affinity capture (SEAC) of lactoferrin"
AUTHOR(S): *Yip, Tai-Tung; Hutchens, T. William*
CORPORATE SOURCE: Department of Food Science and Technology, University of California, Davis, CA, USA
SOURCE: **Experimental Biology and Medicine (Totowa, New Jersey) (1997), 28 (Lactoferrin), 39-58**
CODEN: EBIMFW
PUBLISHER: Humana
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Our ability to identify specific biopolymers and evaluate their structures defines our current potential to understand biol. function. The authors developed new mass spectrometric methods with analyte capture and desorption strategies designed to facilitate the detection and structural anal. of specific biol. marker proteins, even when

present in trace quantities. The authors refer to this method as affinity mass spectrometry (AMS). Affinity mass spectrometry is defined as the design and/or use of mass spectrometric probe element surfaces that have been transformed from inert sample presenting platforms into active affinity capture and release devices. Mass spectrometric probes were prepared with SEAC of lactoferrin. The goal of this investigation was to design and produce new classes of active probe elements for laser desorption time-of-flight mass spectrometry such that the disposable probe elements have surface characteristics that are optimized for DNA- or Ig-based lactoferrin capture and subsequent desorption/ionization for detection/characterization by time-of-flight mass spectrometry. With this new technol., the authors achieve the fast and sensitive detection and characterization (e.g., structural intactness and metal ion binding status) of lactoferrin in various unfractionated biol. samples. The authors also evaluated SEAC probe elements to capture or dock predetd. nos. of lactoferrin mols. in predefined areas of the probe element surface to automate quant. assessments. Enzymic and chemical modifications were performed on the tethered lactoferrin left on the probe surface after the initial mass spectrometric anal. The authors further improved lactoferrin detection sensitivity by thousands of folds by amplifying the bound lactoferrin signal with coupled enzyme reaction. AMS probes with SEAC can also be designed for the detection of cell surface lactoferrin receptors or markers of cellular responses to lactoferrin with equal sensitivity.REFERENCE COUNT: 18

L7 ANSWER 8 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:7085 CAPLUS
DOCUMENT NUMBER: 126:130281
TITLE: Cryptic antigenic determinants on the extracellular pyruvate dehydrogenase complex/mimeotope found in primary biliary cirrhosis. A probe by affinity mass spectrometry
AUTHOR(S): Yip, Tai-Tung; Van de Water, Judy; Gershwin, M. Eric; Coppel, Ross L.; Hutchens, T. William
CORPORATE SOURCE: Dep. Food Sci. Technol., Univ. California Davis, Sch. Med., Davis, CA, 95616, USA
SOURCE: Journal of Biological Chemistry (1996), 271(51), 32825-32833
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Affinity mass spectrometry (AMS) was used to evaluate the structural diversity of the E2 component of pyruvate dehydrogenase complex (PDC) in normal and diseased liver cells, including those from patients with the autoimmune disease primary biliary cirrhosis (PBC). Two different antibodies to PDC-E2, the immunodominant mitochondrial autoantigen in patients with PBC, were used. AMS was performed directly on frozen liver sections and purified bile duct epithelial cells. Mass spectrometric signals associated with the mol. recognition of PBC-specific antigenic determinants were enhanced by an in situ enzyme-linked signal amplification process. Samples from patients with PBC gave strong pos. signals for the antigen(s) recognized by

the monoclonal antibody C355.1. Conversely, tissues from normal and disease controls showed only a minimal signal. AMS was used to identify specific antigenic determinants within the E2 component of PDC for comparison with unknown antigenic determinants observed by affinity capture with C355.1 monoclonal antibody from PBC samples. PDC components bound to C355.1 were mapped and identified by mass before dissociation from the E2 component. A similar approach was used to identify unknown antigenic determinants associated with PBC. The authors believe AMS may be an important new approach with wide application to the identification of mols. associated with a number of disease states.

L7 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1993:576946 CAPLUS
DOCUMENT NUMBER: 119:176946
TITLE: "New desorption strategies for the mass-spectrometric analysis of macromolecules"
AUTHOR(S): *Hutchens, T. William; Yip, Tai Tung*
CORPORATE SOURCE: Dep. Pediatr., Baylor Coll. Med., Houston, TX, 77030, USA
SOURCE: **Rapid Communications in Mass Spectrometry (1993), 7(7), 576-80**
CODEN: RCMSEF; ISSN: 0951-4198
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Two new desorption strategies are based on the mol. design and construction of two general classes of sample 'probe' surfaces. The first class of surfaces is designed to enhance the desorption of intact macromols. presented alone (neat) to the surface; the authors call this surface-enhanced neat desorption (SEND). The availability of probe surfaces derivatized with, or composed of, multiple types and defined nos. of energy-absorbing mols. will facilitate investigations of energy transfer and desorption/ionization mechanisms. The second class of probe surfaces is designed to enhance the desorption of specific macromols. captured directly from unfractionated biol. fluids and exts.; the authors call this surface-enhanced affinity capture (SEAC). Use of these new probe surfaces as chemical defined solid-phase reaction centers will facilitate protein discovery through mol. recognition in situ and also macromol. structure anal. through the sequential chemical and/or enzymic modification of the adsorbed analyte in situ. Specific examples of laser-assisted SEND and SEAC time-of-flight mass spectrometry are presented to illustrate the potential for increased selectivity, analyte detection sensitivity, and mass measurement accuracy.

L9 ANSWER 23 OF 66 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:187654 CAPLUS
DOCUMENT NUMBER: 139:257512
TITLE: "High affinity capture surface for matrix-assisted laser desorption/ionisation compatible protein microarrays"
AUTHOR(S): *Koopmann, Jens-Oliver; Blackburn, Jonathan*
CORPORATE SOURCE: Procognia Ltd, Babraham, CB2 4AT, UK
SOURCE: **Rapid Communications in Mass Spectrometry (2003), 17(5), 455-462**
CODEN: RCMSEF; ISSN: 0951-4198

PUBLISHER: John Wiley & Sons Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A surface for the capture of biotin-tagged proteins on matrix-assisted laser desorption/ionization (MALDI) targets has been investigated. Binding of a poly-L-lysine poly(ethylene glycol)-biotin polymer to glass and gold surfaces has been demonstrated using dual wavelength interferometry. Biotinylated proteins were captured onto this surface using tetrameric neutravidin as a multivalent bridging mol. Biotin tagging of proteins was achieved by chemical biotinylation or by expressing a protein with a biotinylation consensus sequence in E. coli. The specificity of the surface for biotin-tagged proteins allowed the purification of biotin-tagged glutathione-S-transferase from a bacterial lysate directly onto a MALDI target. Subsequently, the protein was digested on the MALDI target and a protein fingerprint anal. confirmed its presence directly, but no E. coli proteins were detected. Therefore, we conclude that this surface is highly specific for the capture of biotin-labeled proteins and has low non-specific binding properties for non-biotinylated proteins. Furthermore, protein-protein interactions using biotinylated lectins were investigated, and the selective capture of the glycoprotein fetuin with wheat germ agglutinin was demonstrated. Also, immobilized Arachis hypogea agglutinin recognized a minor asialo component of this glycoprotein on the array. The high affinity immobilization of proteins onto this surface allowed effective desalting procedures to be used which improved the desorption of high mol. weight proteins. Another aspect of this surface is that a highly ordered coupling of the analyte can be achieved which eliminates the search for the sweet spot and allows the creation of densely packed protein microarrays for use in mass spectrometry.REFERENCE COUNT: 20

L9 ANSWER 38 OF 66 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:199468 CAPLUS
DOCUMENT NUMBER: 136:291190
TITLE: "A mass spectrometry based direct-binding assay for screening binding partners of proteins"
AUTHOR(S): *Zou, Hanfa; Zhang, Qingchun; Guo, Zhong; Guo, Baochuan; Zhang, Qiang; Chen, Xiaoming*
CORPORATE SOURCE: National Chromatographic R&A Center Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Dalian, 116011, Peop. Rep. China
SOURCE: **Angewandte Chemie, International Edition (2002), 41(4), 646-648**
CODEN: ACIEF5; ISSN: 1433-7851
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A novel on-probe direct-binding assay has been developed to screen the binding partners of a target protein. In this assay, the porous silicon probe captures the binding partner of the immobilized protein and serves as the substrate for direct laser desorption/ionization, thereby eliminating the matrix-related background problems. This assay does not need fluorescence tags, radioactive markers, or even prior purifn . Its major application is in the drug discovery process and its strength may be particularly useful in high-throughput screening of lead-drug candidates. It can be used to screen

large compound libraries and to fish the active ingredients present in natural products such as Chinese medicines. The directed binding assay presented may not be limited to the study or protein targets and may be modified to study the binding partners of other biomols., including DNA, RNA, antibodies, lipids, peptides, and whole cells. This assay can be upgraded to a chip-based assay in which several proteins or other biomols. are immobilized on the same probe to search for lead drug candidates for multiple targets.
REFERENCE COUNT: 20

L9 ANSWER 56 OF 66 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:711900 CAPLUS
DOCUMENT NUMBER: 132:75560
TITLE: Affinity Mass Spectrometry-Based Approaches for the Analysis of Protein-Protein Interaction and Complex Mixtures of Peptide-Ligands
AUTHOR(S): Rudiger, Angelika-Heike; Rudiger, Manfred; Carl, Uwe D.; Chakraborty, Trinad; Roepstorff, Peter; Wehland, Jurgen
CORPORATE SOURCE: Department of Cell Biology, Gesellschaft fur Biotechnologische Forschung, Braunschweig, D-38124, Germany
SOURCE: Analytical Biochemistry (1999), 275(2), 162-170
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Combined applications of affinity purification procedures and mass-spectrometric analyses (affinity mass spectrometry or affinity-directed mass spectrometry) have gained broad interest in various fields of biol. sciences. We have extended these techniques to the purification and anal. of closely related peptides from complex mixts. and to the characterization of binding motifs and relative affinities in protein-protein interactions. The posttranslational modifications in the carboxy-terminal region of porcine brain tubulin are used as an example for the applicability of affinity mass spectrometry in the characterization of complex patterns of related peptides. We also show that affinity mass spectrometry allows the mapping of sequential binding motifs of two interacting proteins. Using the ActA/Mena protein-protein complex as a model system, we show that we can selectively purify Mena-binding peptides from a tryptic digest of ActA. The results from this assay are compared to data sets obtained earlier by classical methods using synthetic peptides and mol. genetic expts. As a further expansion of affinity mass spectrometry, we have established an internally standardized system that allows comparison of the affinities of related ligands for a given protein. Here the affinities of two peptide ligands for the monoclonal tubulin-specific antibody YL1/2 are determined in terms of half-maximal competition. (c) 1999 Academic Press. REFERENCE COUNT: 45

L15 ANSWER 7 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:293956 CAPLUS
DOCUMENT NUMBER: 136:321679
TITLE: "Methods for characterizing molecular interactions using affinity capture tandem mass spectrometry"
INVENTOR(S): *Weinberger, Scot; Morris, Tina*

PATENT ASSIGNEE(S): Ciphergen Biosystems, Inc., USA; Human Genome Sciences, Inc.
SOURCE: PCT Int. Appl., 86 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
PATENT NO. KIND DATE APPLICATION NO. DATE
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WO 2002031484 A2 20020418 WO 2000-US28261 20001012
WO 2002031484 C1 20030904
AU 2001011995 A5 20020422 AU 2001-11995 20001012
EP 1327151 A2 20030716 EP 2000-973492 20001012
US 2003219731 A1 20031127 US 2003-406023 20030401
PRIORITY APPLN. INFO.: WO 2000-US28261 A 20001012
AB The invention provides an anal. instrument comprising an affinity capture probe interface, a laser desorption ionization source, and a tandem mass spectrometer. Also presented are new methods for protein discovery and identification and for characterization of mol. interactions that utilize the instrument of the present invention.

L15 ANSWER 8 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:214886 CAPLUS
DOCUMENT NUMBER: 136:243974
TITLE: Sample support with repeating units for mass spectrometric analysis of biomolecules, method for preparation and usage
INVENTOR(S): Schuerenberg, Martin; Franzen, Jochen
PATENT ASSIGNEE(S): Bruker Daltonik G.m.b.H., Germany
SOURCE: Ger. Offen., 8 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
PATENT NO. KIND DATE APPLICATION NO. DATE
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DE 10043042 A1 20020321 DE 2000-10043042 20000901
DE 10043042 C2 20030417
US 2002045270 A1 20020418 US 2001-943076 20010830
GB 2370114 A1 20020619 GB 2001-21196 20010831
PRIORITY APPLN. INFO.: DE 2000-10043042 A 20000901
AB The invention concerns a plane sample support for mass spectrometric anal. of biomols., especially for MALDI technique, that has a microtiterplate-like structure; the sample-holding spots are hydrophilic with affinity areas and are separated by lipophilic rims; the aqueous bio-sample is applied onto the hydrophilic spots and the target mols. are absorbed by the affinity sorbent area; samples are washed on the support plate, and dryed. The eluent solution (e.g.acetonitrile-water) that contains the matrix substance is than applied onto the sample spots, dried and is ready for MALDI anal. The sample support is prepared by screen printing. REFERENCE COUNT: 1

L15 ANSWER 11 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:509127 CAPLUS
DOCUMENT NUMBER: 131:280764
TITLE: "Affinity liquid membrane introduction mass spectrometry"
AUTHOR(S): *Johnson, R. C.; Koch, K.; Graham Cooks, R.*
CORPORATE SOURCE: Chemistry Department, Purdue University, West Lafayette, IN, USA
SOURCE: **Analytica Chimica Acta (1999), 395(3), 239-249**
CODEN: ACACAM; ISSN: 0003-2670
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A mass-spectrometer membrane introduction system, modeled after affinity chromatog., uses chemical modified low vapor-pressure liqs. to selectively bind and release aryl aldehydes from multicomponent aqueous sample streams. Polyphenyl ether, a slightly polar liquid, was admixed with an optimum loading of 10% octadecylamine (weight/weight) and coated on a microporous support to create a hydrophobic, semipermeable membrane containing primary amine functionalities. A 1.9-cm2 surface-area membrane interface was built inhouse for these expts. and optimized for temperature (71°), flow rate (1 mL/min), additive loading, and thickness (0.10 mm). Benzaldehyde was selectively bound to this membrane under standard operating conditions with an efficiency of .apprx.50%, defined as analyte response during release from the membrane (pH 1) as compared to response during loading (pH 7.8). Analytes were introduced into an ion-trap mass spectrometer in a helium stream via a jet separator. Total anal. periods were .apprx.20 min for concns. between 50 ppb and 50 ppm, with a standard deviation of 7% for similar concentration samples. Selective liquid-membrane interfaces represent new technol. for membrane introduction mass spectrometry. REFERENCE COUNT: 41

L15 ANSWER 12 OF 12 CAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:277676 CAPLUS
DOCUMENT NUMBER: 129:36041
TITLE: "Screening for inhibitors of dihydrofolate reductase using pulsed ultrafiltration mass spectrometry"
AUTHOR(S): *Nikolic, Dejan; van Breemen, Richard B.*
CORPORATE SOURCE: Department of Medicinal Chemistry and Pharmacognosy, College of Pharmacy, University of Illinois at Chicago, Chicago, IL, 60612-7231, USA
SOURCE: **Combinatorial Chemistry and High Throughput Screening (1998), 1(1), 47-55**
CODEN: CCHSFU; ISSN: 1386-2073PUBLISHER: Bentham Science Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A method of screening combinatorial libraries for inhibitors of eukaryotic dihydrofolate reductase has been developed using pulsed ultra-filtration electrospray mass spectrometry, which is a continuous-flow affinity separation system for extracting and identifying high affinity ligands in combinatorial libraries. In this application, pulsed ultrafiltration conditions were optimized for the isolation and identification of inhibitors

of dihydrofolate reductase from a 22 compound library containing six known inhibitors of the enzyme including trimethoprim, aminopterin, methotrexate, pyrimethamine, folic acid, and folinic acid, and 16 compds. without known affinity. In order to optimize the screening method, sources of non-specific binding were identified and minimized. A significant source of non-specific binding for this set of library compds. was hydrophobic interaction with the surfaces of the ultrafiltration chamber. After affinity separation of bound (high affinity) vs. free (low affinity) library compds. during pulsed ultrafiltration, receptor-bound ligands were released and eluted using either organic solvent or acidified mobile phase. Although 80% methanol easily disrupted the receptor-ligand complexes, organic solvent had the undesirable effect of releasing non-specifically bound compds. from the chamber and thereby increasing the background noise. Interference from non-specific binding was minimized by releasing bound ligands using a low pH mobile phase eluent instead of organic solvent. Under the conditions used, pulsed ultrafiltration mass spectrometry selectively identified the two library compds. with the highest affinity for dihydrofolate reductase, methotrexate and aminopterin.
REFERENCE COUNT: 14